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U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/578,203 23432 COOPER & DUNHAM, LLP 30 Rockefeller Plaza 20th Floor NEW YORK, NY 10112	Kausik Si	68103-PCT-US/JPW/CH
		INTERNATIONAL APPLICATION NO.
		PCT/US04/36781
I.A. FILING DATE	PRIORITY DATE	
11/05/2004	11/07/2003	

CONFIRMATION NO. 5211
371 FORMALITIES LETTER



OC000000042628811

Date Mailed: 07/19/2010

NOTIFICATION OF DEFECTIVE RESPONSE

The following items have been submitted by the applicant or the IB to the United States Patent and Trademark Office as a Designated Office (37 CFR 1.494):

- Indication of Small Entity Status
- Priority Document
- Copy of the International Application filed on 05/04/2006
- Copy of the International Search Report filed on 05/04/2006
- Copy of IPE Report filed on 05/04/2006
- Preliminary Amendments filed on 05/04/2006
- Information Disclosure Statements filed on 05/04/2006
- Biochemical Sequence Diskette filed on 06/01/2010
- Oath or Declaration filed on 03/21/2007
- Biochemical Sequence Listing filed on 04/29/2010
- Small Entity Statement filed on 05/04/2006
- Request for Immediate Examination filed on 05/04/2006
- Copy of references cited in ISR filed on 05/04/2006
- U.S. Basic National Fees filed on 05/04/2006
- Assignment filed on 03/27/2007
- Priority Documents filed on 05/04/2006
- Specification filed on 05/04/2006
- Claims filed on 05/04/2006
- Abstracts filed on 05/04/2006
- Drawings filed on 05/04/2006

Sequence Listing 3rd Ext Due 7-26-10
 4th Ext 8-26-10
 Deadline 9-26-10

Applicant's response filed 06/01/2010 is hereby acknowledged. The following requirements set forth in the NOTIFICATION of MISSING REQUIREMENTS mailed 02/26/2010 have not been completed.

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d). Refer to attachment or PAIR document dated 07/07/10.

Applicant is required to complete the response within a time limit of ONE MONTH from the date of this Notification or within the time remaining in the response set forth in the Notification of Missing Requirements, whichever is the longer. No extension of this time limit may be granted under 37 CFR 1.136, but the period for response set in the Notification of Missing Requirements may be extended under 37 CFR 1.136(a).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- **For Rules Interpretation, call (571) 272-0951**
- **For Patentin Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.**
- **Send e-mail correspondence for Patentin Software Program Help @ ebc@uspto.gov**

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

Registered users of EFS-Web may alternatively submit their reply to this notice via EFS-Web.

<https://sportal.uspto.gov/authenticate/AuthenticateUserLocalEPF.html>

For more information about EFS-Web please call the USPTO Electronic Business Center at **1-866-217-9197** or visit our website at <http://www.uspto.gov/ebc>.

If you are not using EFS-Web to submit your reply, you must include a copy of this notice.

DONNA S GREENE

Telephone: (703) 756-1408

SEQUENCE LISTINGS AND TABLES RELATED THERETO IN INTERNATIONAL APPLICATIONS FILED IN THE U.S. RECEIVING OFFICE

The Administrative Instructions (AIs) under the Patent Cooperation Treaty (PCT), in force as of **July 1, 2009**, contain important changes relating to the manner of filing, and applicable fees for, sequence listings and/or tables related thereto (sequence-related tables) in international applications. The complete text may be accessed at <http://www.wipo.int/pct/en/texts/index.htm>.

Effective July 1, 2009, Part 8 and Annex C-*bis* will no longer form part of the AIs. Part 8 was introduced in 2001 as a temporary solution to problems arising from the filing of very large sequence listings on paper and provided for a *sequence listing forming part of the international application* to be filed in electronic form on physical medium (e.g., CD), together with the remainder of the application on paper. In 2002, Part 8 was expanded to include sequence-related tables and Annex C-*bis* was added to provide technical requirements. All applicants may now file complete international applications in electronic form, eliminating the need for these temporary provisions.

I. AIS PART 8 AND ANNEX C-BIS DELETED AS OF JULY 1, 2009

- A) **Sequence-related tables cannot be filed as a separate part of the description or in text format.** They must be provided as an integral part of the international application either:
 - in PDF format as part of an international application filed in electronic form via EFS-Web; or
 - on paper as part of an international application filed on paper.
- B) **A sequence listing forming part of an international application** may be provided either:
 - in electronic form, as part of an international application filed in electronic form via EFS-Web, in
 - Annex C/ST.25 text format (preferred), or
 - PDF format; or
 - on paper as part of an international application filed on paper.
- C) **A sequence listing not forming part of the international application (for search under PCT Rule 13ter) in Annex C/ST.25 text format**
 - is not required where the *sequence listing forming part of the international application* was filed in Annex C/ST.25 text format as part of an international application filed in electronic form via EFS-Web
 - is required for search where the *sequence listing forming part of the international application* was filed in PDF
 - is required for search on physical medium (e.g., CD) where the *sequence listing forming part of the international application* was filed on paper as part of an international application filed on paper.

II. CALCULATION OF THE INTERNATIONAL FILING FEE AND FEE REDUCTION UNDER AI § 707

- A) **A sequence-related table** must form an integral part of the international application and will incur FULL page fees with no upper limit.
- B) **A sequence listing forming part of an international application** filed:
 - via EFS-Web in Annex C/ST.25 text format will incur NO page fees;
 - on paper or in PDF format will incur FULL page fees with no upper limit.

III. AVAILABILITY OF SEQUENCE LISTINGS SUBMITTED FOR SEARCH UNDER PCT RULE 13TER

International Searching Authorities will be required to transmit to the International Bureau a copy of an Annex C/ST.25 text format sequence listing provided for search under PCT Rule 13ter. Any such sequence listing will be made available on PATENTSCOPE® (*sequence listings forming part of the international application* are already available).

IV. JULY 2009 REQUEST (PCT/RO/101)

The Request now has two options for the last sheet: one for paper filings; and one for EFS-Web filings. The July 2009 Request may be accessed at <http://www.wipo.int/pct/en/forms/index.htm>.

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=7; day=7; hr=10; min=16; sec=5; ms=464;]

=====

Reviewer Comments:

<210> 1

<211> 78

<212> DNA

<213> S. cerevisiae

<400> 1

GGAAT TCGGC ACCAT GTGCT TCTGT AAATA GTGTA TTGTG TTTT AATGT 50
TGGAC TGGTT GGAAT AAAGC TCTAG AGC 78

For SEQ ID # 1 through 30 , "37 CFR 1.822 (c) Format representation of nucleotides. (1) A nucleotide sequence shall be listed using the lower-case letter for representing the one-letter code for the nucleotide bases set forth in WIPO Standard ST.25 (1998) Appendix 2, Table 1." Please make all necessary changes.

Nucleotide bases must be in groups of ten nucleotides, and maximum of 60 per line.

<210> 2

<211> 27

<212> DNA

<213> Artificial sequence

<223> Primer directed to Aplysia cDNA

<400> 2

GCGGA ATTCA TNSAR GTNAT HCCNT GG

If the Numeric identifier <213> is "Artificial" there should be mandatory feature inserted which consists of numeric identifiers <220>, <221>, <222>, and <223>. Numeric identifier "<220> feature" should remain blank, numeric Identifier "<221> Name/Key" should be selected from "WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6," numeric identifier "<222> Location" should "Specify location within sequence," and numeric identifier "<223> Other Information" should provide "Other relevant information, four lines maximum."

The sequence rules require that "the enumeration of nucleotide bases shall start at the first base of the sequence with 1. The enumeration shall be continuous through the whole sequence in the direction 5' to 3'. The enumeration shall be marked in the right margin, next to the line containing the one-letter codes for bases, and giving the number of the last base of that line." The enumeration is not marked in the right margin. Please check for the similar errors as sample shown above and make all necessary corrections.

Application No: 10578203 Version No: 1.0

Input Set:

Output Set:

Started: 2010-06-18 15:39:43.338
Finished: 2010-06-18 15:40:05.747
Elapsed: 0 hr(s) 0 min(s) 22 sec(s) 409 ms
Total Warnings: 762
Total Errors: 75
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 112	Upper case found in data; Found at position(0) SeqId(1)
W 112	Upper case found in data; Found at position(1) SeqId(1)
W 112	Upper case found in data; Found at position(2) SeqId(1)
W 112	Upper case found in data; Found at position(3) SeqId(1)
W 112	Upper case found in data; Found at position(4) SeqId(1)
W 112	Upper case found in data; Found at position(5) SeqId(1)
W 112	Upper case found in data; Found at position(6) SeqId(1)
W 112	Upper case found in data; Found at position(7) SeqId(1)
W 112	Upper case found in data; Found at position(8) SeqId(1)
W 112	Upper case found in data; Found at position(9) SeqId(1)
W 112	Upper case found in data; Found at position(10) SeqId(1)
W 112	Upper case found in data; Found at position(11) SeqId(1)
W 112	Upper case found in data; Found at position(12) SeqId(1)
W 112	Upper case found in data; Found at position(13) SeqId(1)
W 112	Upper case found in data; Found at position(14) SeqId(1)
W 112	Upper case found in data; Found at position(15) SeqId(1)
W 112	Upper case found in data; Found at position(16) SeqId(1)
W 112	Upper case found in data; Found at position(17) SeqId(1)
W 112	Upper case found in data; Found at position(18) SeqId(1)

Input Set:

Output Set:

Started: 2010-06-18 15:39:43.338
Finished: 2010-06-18 15:40:05.747
Elapsed: 0 hr(s) 0 min(s) 22 sec(s) 409 ms
Total Warnings: 762
Total Errors: 75
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
W 112	Upper case found in data; Found at position(19) SeqId(1) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (2)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 27 SEQID(2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (3)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 26 SEQID(3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (4)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 21 SEQID(4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (5)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 20 SEQID(5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (6)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)

Input Set:

Output Set:

Started: 2010-06-18 15:39:43.338
Finished: 2010-06-18 15:40:05.747
Elapsed: 0 hr(s) 0 min(s) 22 sec(s) 409 ms
Total Warnings: 762
Total Errors: 75
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (7)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 27 SEQID(7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (8)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 26 SEQID(8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (9)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 21 SEQID(9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (10)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (11)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (12)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 21 SEQID(12)

Input Set:

Output Set:

Started: 2010-06-18 15:39:43.338
Finished: 2010-06-18 15:40:05.747
Elapsed: 0 hr(s) 0 min(s) 22 sec(s) 409 ms
Total Warnings: 762
Total Errors: 75
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (13)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 22 SEQID(13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (14)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 35 SEQID(14)
E 253	The number of bases differs from <211> Input: 37 Calculated:35
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (15)
E 330	Invalid protein , found in SEQID(15) POS (1) Invalid Protein:CGGGA
E 330	Invalid protein , found in SEQID(15) POS (2) Invalid Protein:TCCAT
E 330	Invalid protein , found in SEQID(15) POS (3) Invalid Protein:GCTGG
E 330	Invalid protein , found in SEQID(15) POS (4) Invalid Protein:ACAGC
E 330	Invalid protein , found in SEQID(15) POS (5) Invalid Protein:AACAA
E 330	Invalid protein , found in SEQID(15) POS (6) Invalid Protein:CAG
E 253	The number of bases differs from <211> Input: 28 Calculated:0
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (16)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 31 SEQID(16)

Input Set:

Output Set:

Started: 2010-06-18 15:39:43.338
Finished: 2010-06-18 15:40:05.747
Elapsed: 0 hr(s) 0 min(s) 22 sec(s) 409 ms
Total Warnings: 762
Total Errors: 75
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (17)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 26 SEQID(17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (18)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 41 SEQID(18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (19)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 41 SEQID(19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (20)
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 25 SEQID(20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21) This error has occurred more than 20 times, will not be displayed
E 224	<220>,<223> section required as <213> has Artificial sequence or Unknown in SEQID (21) This error has occurred more than 20 times, will not be displayed
E 254	The total number of bases conflicts with running total Input: 0, Calculated : 24 SEQID(21)
E 331	Count of Protein differs from the <211> tag Input: 17
E 254	The total number of bases conflicts with running total Input: 0,

Input Set:

Output Set:

Started: 2010-06-18 15:39:43.338
Finished: 2010-06-18 15:40:05.747
Elapsed: 0 hr(s) 0 min(s) 22 sec(s) 409 ms
Total Warnings: 762
Total Errors: 75
No. of SeqIDs Defined: 30
Actual SeqID Count: 30

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 330	Invalid protein , found in SEQID(29) POS (1) Invalid Protein:TTTGA
E 330	Invalid protein , found in SEQID(29) POS (2) Invalid Protein:GCATT
E 330	Invalid protein , found in SEQID(29) POS (3) Invalid Protein:CTGGC
E 330	Invalid protein , found in SEQID(29) POS (4) Invalid Protein:TTC
E 253	The number of bases differs from <211> Input: 18 Calculated:0
E 330	Invalid protein , found in SEQID(30) POS (1) Invalid Protein:AAACA
E 330	Invalid protein , found in SEQID(30) POS (2) Invalid Protein:GAGCA
E 330	Invalid protein , found in SEQID(30) POS (3) Invalid Protein:GGTCC
E 330	Invalid protein , found in SEQID(30) POS (4) Invalid Protein:CGGCA
E 330	Invalid protein , found in SEQID(30) POS (5) Invalid Protein:GAAAT
E 330	Invalid protein , found in SEQID(30) POS (6) Invalid Protein:AGT
E 253	The number of bases differs from <211> Input: 28 Calculated:0

<110> Kausik Si and Eric Kandel
<120> Prion-like form of CPEB and related compositions and methods
<130> 68103/JPW/BJA
<140> 10578203
<141> 2010-06-18
<150> PCT/US04/36781
<151> 2004-11-05
<150> 60/518,385
<151> 2003-11-07
<160> 30
<170> PatentIn version 3.3
<210> 1
<211> 78
<212> DNA
<213> S. cerevisiae
<400> 1

GGAAT TCGGC ACCAT GTGCT TCTGT AAATA GTGTA TTGTG TTTTT AATGT 50
TGGAC TGGTT GGAAT AAAGC TCTAG AGC 78

<210> 2
<211> 27
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia cDNA
<400> 2

GCGGA ATTCA TNSAR GTNAT HCCNT GG

<210> 3
<211> 26
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia cDNA
<400> 3

GCGGG ATCCT GNTGC CANTS CCARC A

<210> 4
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia mRNA

<400> 4

CACTG TCTTG TTCGA CTCCA G

<210> 5
<211> 20
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia mRNA
<400> 5

AACAC ATGGT TACTG TCCGC

<210> 6
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia mRNA

<400> 6

CATGA AAGCC GTGCA AGCTG CATT

<210> 7
<211> 27
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA and cDNA

<400> 7

CGGGA TCCAT GTACA ACAAA TTTGT TA

<210> 8
<211> 26
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 8

TCCCC GCGGC GATCC TCCGC CTCCT C

<210> 9
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 9

ATGGA CTCGC TCAAG TTACC A

<210> 10
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 10

CGCGA TGCCT GATTG ATTGT TGAA

<210> 11
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 11

TGTGC GTTAT TTTAT CGTTT AGTG

<210> 12
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 12

GACTT CATCC GCCAC CAGTC G

<210> 13
<211> 22
<212> DNA
<213> Artificial sequence
<223> Primer directed to Drosophila melanogaster mRNA

<400> 13

CACCA GGAAC TTCTT GAATC CG

<210> 14
<211> 37
<212> DNA
<213> Artificial sequence
<223> Primer directed to *Drosophila melanogaster* cDNA

<400> 14

CCCTC GAGAA GCTTT TAACA CCAGC GAAAG GGGAC

<210> 15
<211> 28
<212> DNA
<213> Artificial sequence
<223> Primer directed to *Drosophila melanogaster* cDNA

<400> 15

CGGGA TCCAT GCTGG ACAGC AACAA CAG

<210> 16
<211> 31
<212> DNA
<213> Artificial sequence
<223> Primer directed to *Drosophila melanogaster* cDNA

<400> 16

GACTA GTCTA GAATA GATTA GCAAA GAAAT C

<210> 17
<211> 26
<212> DNA
<213> Artificial sequence
<223> Primer directed to *Aplysia neuronal actin* cDNA

<400> 17

GGGAA TTCGT CTGGA GCCAC CAACA C

<210> 18
<211> 41
<212> DNA
<213> Artificial sequence

<223> Primer directed to Aplysia neuronal actin

<400> 18

CGGAT CCATT TATTA ACATT GTATA AAAAA TACAG TTGAA C

<210> 19

<211> 41

<212> DNA

<213> Artificial sequence

<223> Primer directed to Aplysia neuronal actin

<400> 19

CGGAT CCATT TATTA ACATT GTATG GGAAA TACAG TTGAA C

<210> 20

<211> 25

<212> DNA

<213> Artificial sequence

<223> Primer directed to Aplysia CPEB cDNA

<400> 20

CGGGA TCCAT GCAAG CCATG GCCGT

<210> 21

<211> 24

<212> DNA

<213> Artificial sequence

<223> Primer directed to Aplysia CPEB cDNA

<400> 21

TCCCC GCGGT GGACC AGGCG TGTA

<210> 22

<211> 17

<212> PRT

<213> Artificial sequence

<223> C-terminal peptide of CPEB (CPEB77)

<400> 22

LCNSH QGNYF CRDLL CF

<210> 23

<211> 30
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia RNA

<400> 23

GCGAG CTCCG CGGCC GCGTT TTTTT TTTTT

<210> 24
<211> 21
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia sensorin RNA

<400> 24

AACAG AAACA GTCTT TCCCC C

<210> 25
<211> 19
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia sensorin RNA

<400> 25

TCTTG ACTCA CCAAC TGCC

<210> 26
<211> 24
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia Bmp1 RNA

<400> 26

ATCTA TCGCC TATTA TTATC ACCA

<210> 27
<211> 20
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia Bmp1 RNA

<400> 27

ATCCC ATGCA TTTGT TTGTT

<210> 28
<211> 17
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia N-actin RNA

<400> 28

CCCAT CCATT GTCCA CA

<210> 29
<211> 18
<212> DNA
<213> Artificial sequence
<223> Primer directed to Aplysia N-actin RNA

<400> 29

TTTGA GCATT CTGGC TTC

<210> 30
<211> 28
<212> DNA
<213> Artificial sequence
<223> Antisense oligo directed to Aplysia CPEB mRNA

<400> 30

AAACA GAGCA GGTCC CGGCA GAAAT AGT

EXHIBIT B